

1984 TAGGAGTGGGCTTCTGGATCAAAAGGCAATTCATTTGGAGTTTCTAAAGCATCTCCA 1743

LOCATION: (101753)...(101996)
 NAME/KEY: CDS
 LOCATION: (110324)...(110439)
 NAME/KEY: CDS
 LOCATION: (124058)...(124278)
 NAME/KEY: CDS
 LOCATION: (127009)...(127130)
 NAME/KEY: CDS
 LOCATION: (128910)...(129139)
 US-09-426-290-1

Query Match 14.2% Score 408.6. PR 4: Length 164575;
 Best Local Similarity 69.6%; Pred. No. 8e-96;
 Matches 585; Conservative 0; Mismatches 249; Indels 7; Gaps 2;

QY 1390 TTCTCAATCCCATATATAGCGTTAGTACTGTATTTATGTTCTTCCTGGCTTAC 1449
 DB 166669 TTTTAAATTTTAAATAGAAATAGAAATAGAAATAGAAATAGAAATAG 160610
 QY 1450 TTCACTGTAATATAGAGTCACTTTCACCTCATAGAGTCAATGATTTAT 1509
 DB 160609 TTATCTGAAATGATGATTTCCAAATTCATTCATTCATTCATTCATTC 160530
 QY 1510 CTTTAAATGCTGAGTAATATCCCATTTGTAATATGATTCAGCTTTTAT 1569
 DB 160549 CTTTAAATGCTGAGTAATATCCCATTTGTAATATGATTCAGCTTTTAT 160490
 QY 1570 ATCTGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 1629
 DB 160489 TATATATTTTAAATAGAAATAGAAATAGAAATAGAAATAGAAATAG 160430
 QY 1630 GAAATAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1683
 DB 160429 AAACATACCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160370
 QY 1684 CAGCAGTGGGTTGCTGATATAGAGTCACTGAGTCACTGAGTCACTGAGT 1743
 DB 160369 CAGTATGAGGAGTGGTCAATATGATTTGATTTGATTTGATTTGAT 160310
 QY 1744 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1803
 DB 160309 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160250
 QY 1804 CTTTCTCCACACCTCTCCACATTTATTTGAGATTTGATTCAGCTTCT 1863
 DB 160249 TATTTCTCCACATTTCTCCACATTTGATTTGATTTGATTTGATTT 160190
 QY 1864 GAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1922
 DB 160189 AGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160130
 QY 1923 TCTTGAACATCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGT 1982
 DB 160129 TCTTGAACATCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGT 160070
 QY 1983 ATTACTGCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 2042
 DB 160069 ATTACTGCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 160010
 QY 2043 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 2102
 DB 160009 TATTTCTCCACATTTCTCCACATTTGATTTGATTTGATTTGATTTG 159950
 QY 2103 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 2162
 DB 159949 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 159890
 QY 2163 TTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 2223
 DB 159889 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 159830
 QY 2223 T 2223

DB 159829 T 159829

RESULT 4

US 08 742-185-102

Sequence 102, Application US/08742185

Patent No. 6020476

GENERAL INFORMATION:

APPLICANT: page, David C.

APPLICANT: Keijio, Kenzo

APPLICANT: Saxena, Nisha

APPLICANT: Hawkins, Trevor

APPLICANT: Reeve, Mary Pat

TITLE OF INVENTION: DAT: A GENE FAMILY ASSOCIATED WITH AZOOPERMIA

NUMBER OF SEQUENCES: 102

CORRESPONDENCE ADDRESS:

ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: Massachusetts

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/742,185

FILING DATE: 30-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/690,734

FILING DATE: 31-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/710,429

FILING DATE: 22-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WH194-07A2

TELEPHONE: (617) 861-6240

TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 102:

SEQUENCE CHARACTERISTICS:

LENGTH: 40328 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-742-185-102

Query Match 23.8% Score 396.6, DB 3, Length 40328;

Best Local Similarity 69.4%; Pred. No. 5.5e-93;

Matches 584; Conservative 0; Mismatches 249; Indels 8; Gaps 3;

QY 1390 TTCTCAATCCCATATATAGCGTTAGTACTGTATTTATGTTCTTCCTGGCTTAC 1449
 DB 166669 TTTTAAATTTTAAATAGAAATAGAAATAGAAATAGAAATAGAAATAG 160610
 QY 1450 TTCACTGTAATATAGAGTCACTTTCACCTCATAGAGTCAATGATTTAT 1509
 DB 160609 TTATCTGAAATGATGATTTCCAAATTCATTCATTCATTCATTCATTC 160530
 QY 1510 CTTTAAATGCTGAGTAATATCCCATTTGTAATATGATTCAGCTTTTAT 1569
 DB 160549 CTTTAAATGCTGAGTAATATCCCATTTGTAATATGATTCAGCTTTTAT 160490
 QY 1570 ATCTGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 1629
 DB 160489 TATATATTTTAAATAGAAATAGAAATAGAAATAGAAATAGAAATAG 160430
 QY 1630 GAAATAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1683
 DB 160429 AAACATACCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160370
 QY 1684 CAGCAGTGGGTTGCTGATATAGAGTCACTGAGTCACTGAGTCACTGAGT 1743
 DB 160369 CAGTATGAGGAGTGGTCAATATGATTTGATTTGATTTGATTTGAT 160310
 QY 1744 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1803
 DB 160309 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160250
 QY 1804 CTTTCTCCACACCTCTCCACATTTATTTGAGATTTGATTCAGCTTCT 1863
 DB 160249 TATTTCTCCACATTTCTCCACATTTGATTTGATTTGATTTGATTT 160190
 QY 1864 GAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 1922
 DB 160189 AGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 160130
 QY 1923 TCTTGAACATCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGT 1982
 DB 160129 TCTTGAACATCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGT 160070
 QY 1983 ATTACTGCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 2042
 DB 160069 ATTACTGCTTTCAGTCTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 160010
 QY 2043 CAGTCTGCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 2102
 DB 160009 TATTTCTCCACATTTCTCCACATTTGATTTGATTTGATTTGATTTG 159950
 QY 2103 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 2162
 DB 159949 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 159890
 QY 2163 TTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGTCACT 2223
 DB 159889 CTTTAAATGCTGAGTCACTGAGTCACTGAGTCACTGAGTCACTGAGT 159830
 QY 2223 T 2223

Matches 597; Conservative 0; Mismatches 260; Indels 17; Caps , 7;

[illegible]

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1 CURRENT APPLICATION NUMBER: US/09/741,150
2
3 CURRENT FILING DATE: 2000-12-21
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5 NUMBER OF SEQ ID NOS: 4
6
7 SOFTWARE: FastSeq for Windows Version 4.0.
8
9 SEQ ID NO 3
10
11 LENGTH: 112132
12
13 TYPE: DNA
14
15 ORGANISM: Human
16
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: (1)...(112132)
20
21 OTHER INFORMATION: n = A,T,C or G
22
23 US-09-741-150-3

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Query Match      12.18%  Score 347.8; DB 4  Length 112132;
Best Local Similarity 64.8%; Pred. No. 4,36-80;
Matches 620; Conservative 0; Mismatches 312; Indels 25; Gaps 6;

QY 1263 ATTTCACATGTTTCATTCGTCACATTTCTCCCAATCTTCCACCCCTCTCCCTCTCCACAGAG 1322
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QY 1323 TCCATTAAGATTTTCATATATGATGATGCTGCTTTCTGCTGCTGATACAGCGGTATATC 1382
DB 71784 CACGCCACCCCAACACAGGCCCCAGTGTGTATTTTCCCTCCGACATGTCGCATGTGTGTG 71843
QY 1383 TACCATCTTCTAAATCCGCAATATATATGCGTATGATACGTATATATGTTTTCGTTCT 1442
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QY 1443 GCGCTACTTACCTCTGTATATATAGGCTCCAGCTTCATCCACGACCATATAGACATTCACA 1502
DB 71900 GCATTAATTTTGTAAGATATAGGCTTATAGTTTATATACATGATCTCCGACGAGCAATG 71959
QY 1503 ATGATATCTTTTAAAGCTGTGAGTAACTGCTCATGTTGATGTATACACAGGTTCTCTA 1562
DB 71960 TCGGCTTCCTTTTATGCGTCGATCATGATTTATCTGCTGTACATGTACACATTTCTCTA 72019
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DB 72020 TCCATTCATTCATTAATATGCGATATTCGGATTAATCATGATTTCTCTATATGATAGT 72079
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DB 72080 CTGATTAATATATATATATATATCT-----CTTTCTCTCTCTATATAT 72124
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DB 72125 CCAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 72184
QY 1743 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 1802
DB 72186 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 72243
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QY 1863 TGAATGATGTAATAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1921
DB 72304 TGACATGCGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 72363
QY 1922 AATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1981
DB 72364 AATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 72422
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DB 72423 TATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 72479
QY 2042 GATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2101
DB 72480 TGATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 72539

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[illegible]

